

SEQUENCE LISTING

<110> Kihara Memorial Yokohama Foundation for the Advancement of Life Sciences

City of Yokohama

<120> TRF2 DNA-binding domain mutant proteins, telomeric DNA mutants, and use of a structure of a complex between a TRF2 DNA binding domain and a double-stranded DNA molecule

<130> FP-047PCT

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<150> JP P2004-046238

<151> 2004-02-23

<160> 29

<170> PatentIn version 3.1

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<212> DNA

<213> Homo sapiens

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<221> CDS

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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
20 25 30

tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg 144
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
35 40 45

atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac 189
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
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<213> Homo sapiens

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Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln Lys Trp Thr Val Glu
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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
20 25 30

Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
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1 5 10 15 48

gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
20 25 30 96

tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
35 40 45 144

atg att aag gat cgc tgg cg^g acc atg aaa aga ctt ggc atg aac
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Trp	Ala	Ala	Ile	Ser	Lys	Asn	Tyr	Pro	Phe	Val	Asn	Arg	Thr	Ala	Val
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1								10							15

gaa	agc	gag	tgg	gtc	aag	gct	gga	gtg	cag	aaa	tat	ggg	gaa	gga	aac
Glu	Ser	Glu	Trp	Val	Lys	Ala	Gly	Val	Gln	Lys	Tyr	Gly	Glu	Gly	Asn
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tgg	tct	gcc	att	tct	aaa	aat	tac	cca	ttt	gtt	aac	cga	aca	gct	gtg
Trp	Ser	Ala	Ile	Ser	Lys	Asn	Tyr	Pro	Phe	Val	Asn	Arg	Thr	Ala	Val
								35	40						45

atg	att	aag	gat	cgc	tgg	cgg	acc	atg	aaa	aga	ctt	ggc	atg	aac
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35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
50 55 60

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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
20 25 30

tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg 144
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
35 40 45

atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac 189
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
20 25 30

Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn
50 55 60

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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
20 25 30

tgg gct gcc att tct aaa aat tac cca ttt gtt aac cga aca gct gtg 144
Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ala Val
35 40 45

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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn
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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac
Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
20 25 30 96

tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg 144

Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
 35 40 45

atg att aag gat cgc tgg cg acc atg aaa aag ctt ggc atg aac 189
 Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn
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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn
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Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val
 35 40 45

Met Ile Lys Asp Arg Trp Arg Thr Met Lys Lys Leu Gly Met Asn
 50 55 60

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gaa agc gag tgg gtc aag gct gga gtg cag aaa tat ggg gaa gga aac 96
 Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn

20	25	30	
tgg tct gcc att tct aaa aat tac cca ttt gtt aac cga aca tct gtg Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val 35 40 45			144
atg att aag gat cgc tgg cgg acc atg aaa aga ctt ggc atg aac Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn 50 55 60			189
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Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys Tyr Gly Glu Gly Asn 20 25 30			
Trp Ser Ala Ile Ser Lys Asn Tyr Pro Phe Val Asn Arg Thr Ser Val 35 40 45			
Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg Leu Gly Met Asn 50 55 60			
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agg cgg gcg tcc cgc agt agc ggg cgg gcc cgg cgg ggg cgc cac gag Arg Arg Ala Ser Arg Ser Ser Gly Arg Ala Arg Arg Gly Arg His Glu			96

20	25	30	
ccg ggg ctg ggg ggc ccg gcg gag cgc ggc gcg ggg gag gca cgg ctg Pro Gly Leu Gly Gly Pro Ala Glu Arg Gly Ala Gly Glu Ala Arg Leu	35	40	144
gaa gag gca gtc aat cgc tgg gtg ctc aag ttc tac ttc cac gag gcg Glu Glu Ala Val Asn Arg Trp Val Leu Lys Phe Tyr Phe His Glu Ala	50	55	192
ctg cgg gcc ttt cgg ggt agc cgg tac ggg gac ttc aga cag atc cgg Leu Arg Ala Phe Arg Gly Ser Arg Tyr Gly Asp Phe Arg Gln Ile Arg	65	70	240
gac atc atg cag gct ttg ctt gtc agg ccc ttg ggg aag gag cac acc Asp Ile Met Gln Ala Leu Leu Val Arg Pro Leu Gly Lys Glu His Thr	85	90	288
gtg tcc cga ttg ctg cgg gtt atg cag tgt ctg tcg cgg att gaa gaa Val Ser Arg Leu Leu Arg Val Met Gln Cys Leu Ser Arg Ile Glu Glu	100	105	336
ggg gaa aat tta gac tgt tcc ttt gat atg gag gct gag ctc aca cca Gly Glu Asn Leu Asp Cys Ser Phe Asp Met Glu Ala Glu Leu Thr Pro	115	120	384
ctg gaa tca gct atc aat gtg ctg gag atg att aaa acg gaa ttt aca Leu Glu Ser Ala Ile Asn Val Leu Glu Met Ile Lys Thr Glu Phe Thr	130	135	432
ctg aca gaa gca gtg gtc gaa tcc agt aga aaa ctg gtc aag gaa gct Leu Thr Glu Ala Val Val Glu Ser Ser Arg Lys Leu Val Lys Glu Ala	145	150	480
gct gtc att att tgt atc aaa aac aaa gaa ttt gaa aag gct tca aaa Ala Val Ile Ile Cys Ile Lys Asn Lys Glu Phe Glu Lys Ala Ser Lys	165	170	528
att ttg aaa aaa cat atg tcc aag gac ccc aca act cag aag ctg aga Ile Leu Lys Lys His Met Ser Lys Asp Pro Thr Thr Gln Lys Leu Arg	180	185	576
aat gat ctc ctg aat att att cga gaa aag aac ttg gcc cat cct gtt Asn Asp Leu Leu Asn Ile Ile Arg Glu Lys Asn Leu Ala His Pro Val	195	200	624
atc cag aac ttt tca tat gag acc ttc cag cag aag atg ctg cgc ttc Ile Gln Asn Phe Ser Tyr Glu Thr Phe Gln Gln Lys Met Leu Arg Phe	210	215	672
ctg gag agc cac ctg gat gac gcc gag ccc tac ctc ctc acg atg gcc Leu Glu Ser His Leu Asp Asp Ala Glu Pro Tyr Leu Leu Thr Met Ala	225	230	720
		235	240

aaa aag gct ttg aaa tct gag tcc gct gcc tca agt aca ggg aag gaa	Lys Lys Ala Leu Lys Ser Glu Ser Ala Ala Ser Ser Thr Gly Lys Glu	768
245	250	255
gat aaa cag cca gca cca ggg cct gtg gaa aag cca ccc aga gaa ccc	Asp Lys Gln Pro Ala Pro Gly Pro Val Glu Lys Pro Pro Arg Glu Pro	816
260	265	270
gca agg cag cta cgg aat cct cca acc acc att gga atg atg act ctg	Ala Arg Gln Leu Arg Asn Pro Pro Thr Thr Ile Gly Met Met Thr Leu	864
275	280	285
aaa gca gct ttc aag act ctg tct ggt gca cag gat tct gag gca gcc	Lys Ala Ala Phe Lys Thr Leu Ser Gly Ala Gln Asp Ser Glu Ala Ala	912
290	295	300
ttt gca aaa ctg gac cag aag gat ctg gtt ctt cct act caa gct ctc	Phe Ala Lys Leu Asp Gln Lys Asp Leu Val Leu Pro Thr Gln Ala Leu	960
305	310	315
320		
cca gca tca cca gcc ctc aaa aac aag aga ccc aga aaa gat gaa aac	Pro Ala Ser Pro Ala Leu Lys Asn Lys Arg Pro Arg Lys Asp Glu Asn	1008
325	330	335
gaa agt tca gcc ccg gct gac ggt gag ggt ggc tcg gaa ctg cag ccc	Glu Ser Ser Ala Pro Ala Asp Gly Glu Gly Ser Glu Leu Glu Gln Pro	1056
340	345	350
aag aac aag cgc atg aca ata agc aga ttg gtc ttg gag gag gac agc	Lys Asn Lys Arg Met Thr Ile Ser Arg Leu Val Leu Glu Glu Asp Ser	1104
355	360	365
cag agt act gag ccc agc gca ggc ctc aac tcc tcc cag gag gcc gct	Gln Ser Thr Glu Pro Ser Ala Gly Leu Asn Ser Ser Gln Glu Ala Ala	1152
370	375	380
tca gcg cca cca tcc aag ccc acc gtt ctc aac caa ccc ctc cct gga	Ser Ala Pro Pro Ser Lys Pro Thr Val Leu Asn Gln Pro Leu Pro Gly	1200
385	390	395
400		
gag aag aat ccc aaa gta ccc aaa ggc aag tgg aac agc tct aat ggg	Glu Lys Asn Pro Lys Val Pro Lys Gly Lys Trp Asn Ser Ser Asn Gly	1248
405	410	415
gtt gaa gaa aag gag act tgg gtg gaa gag gat gaa ctg ttt caa gtt	Val Glu Glu Lys Glu Thr Trp Val Glu Glu Asp Glu Leu Phe Gln Val	1296
420	425	430
cag gca gca cca gat gaa gac agt aca acc aat ata aca aaa aag cag	Gln Ala Ala Pro Asp Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln	1344
435	440	445
aag tgg act gta gaa gaa agc gag tgg gtc aag gct gga gtg cag aaa	Lys Trp Thr Val Glu Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys	1392

450	455	460	
tat ggg gaa gga aac tgg gct gcc att tct aaa aat tac cca ttt gtt Tyr Gly Glu Gly Asn Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val			1440
465	470	475	480
aac cga aca gct gtg atg att aag gat cgc tgg cg ^g acc atg aaa aga Asn Arg Thr Ala Val Met Ile Lys Asp Arg Trp Arg Thr Met Lys Arg			1488
485	490	495	
ctt ggc atg aac Leu Gly Met Asn			1500
500			
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Pro Gly Leu Gly Gly Pro Ala Glu Arg Gly Ala Gly Glu Ala Arg Leu 35 40 45			
Glu Glu Ala Val Asn Arg Trp Val Leu Lys Phe Tyr Phe His Glu Ala 50 55 60			
Leu Arg Ala Phe Arg Gly Ser Arg Tyr Gly Asp Phe Arg Gln Ile Arg 65 70 75 80			
Asp Ile Met Gln Ala Leu Leu Val Arg Pro Leu Gly Lys Glu His Thr 85 90 95			
Val Ser Arg Leu Leu Arg Val Met Gln Cys Leu Ser Arg Ile Glu Glu 100 105 110			
Gly Glu Asn Leu Asp Cys Ser Phe Asp Met Glu Ala Glu Leu Thr Pro 115 120 125			

Leu Glu Ser Ala Ile Asn Val Leu Glu Met Ile Lys Thr Glu Phe Thr
130 135 140

Leu Thr Glu Ala Val Val Glu Ser Ser Arg Lys Leu Val Lys Glu Ala
145 150 155 160

Ala Val Ile Ile Cys Ile Lys Asn Lys Glu Phe Glu Lys Ala Ser Lys
165 170 175

Ile Leu Lys Lys His Met Ser Lys Asp Pro Thr Thr Gln Lys Leu Arg
180 185 190

Asn Asp Leu Leu Asn Ile Ile Arg Glu Lys Asn Leu Ala His Pro Val
195 200 205

Ile Gln Asn Phe Ser Tyr Glu Thr Phe Gln Gln Lys Met Leu Arg Phe
210 215 220

Leu Glu Ser His Leu Asp Asp Ala Glu Pro Tyr Leu Leu Thr Met Ala
225 230 235 240

Lys Lys Ala Leu Lys Ser Glu Ser Ala Ala Ser Ser Thr Gly Lys Glu
245 250 255

Asp Lys Gln Pro Ala Pro Gly Pro Val Glu Lys Pro Pro Arg Glu Pro
260 265 270

Ala Arg Gln Leu Arg Asn Pro Pro Thr Thr Ile Gly Met Met Thr Leu
275 280 285

Lys Ala Ala Phe Lys Thr Leu Ser Gly Ala Gln Asp Ser Glu Ala Ala
290 295 300

Phe Ala Lys Leu Asp Gln Lys Asp Leu Val Leu Pro Thr Gln Ala Leu
305 310 315 320

Pro Ala Ser Pro Ala Leu Lys Asn Lys Arg Pro Arg Lys Asp Glu Asn
325 330 335

Glu Ser Ser Ala Pro Ala Asp Gly Glu Gly Gly Ser Glu Leu Gln Pro
340 345 350

Lys Asn Lys Arg Met Thr Ile Ser Arg Leu Val Leu Glu Glu Asp Ser
355 360 365

Gln Ser Thr Glu Pro Ser Ala Gly Leu Asn Ser Ser Gln Glu Ala Ala
370 375 380

Ser Ala Pro Pro Ser Lys Pro Thr Val Leu Asn Gln Pro Leu Pro Gly
385 390 395 400

Glu Lys Asn Pro Lys Val Pro Lys Gly Lys Trp Asn Ser Ser Asn Gly
405 410 415

Val Glu Glu Lys Glu Thr Trp Val Glu Glu Asp Glu Leu Phe Gln Val
420 425 430

Gln Ala Ala Pro Asp Glu Asp Ser Thr Thr Asn Ile Thr Lys Lys Gln
435 440 445

Lys Trp Thr Val Glu Glu Ser Glu Trp Val Lys Ala Gly Val Gln Lys
450 455 460

Tyr Gly Glu Gly Asn Trp Ala Ala Ile Ser Lys Asn Tyr Pro Phe Val
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